

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 18:23:39; Search time 67 Seconds
(without alignments)
2305.733 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALSLINDFASLSFAE.....LENNKINILSETDRPLQVY 350

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA_QPRT-fastbp -SUFFIX=p2n.rml -MINMATCH=0.1 -LOOPEL=0
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-FPAEXT=7 -FGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:*

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- 2: /cg2.6/ptodata/2/ina/5b.COMB.seq:*
- 3: /cg2.6/ptodata/2/ina/5a.COMB.seq:*
- 4: /cg2.6/ptodata/2/ina/5b.COMB.seq:*
- 5: /cg2.6/ptodata/2/ina/PTDS.COMB.seq:*
- 6: /cg2.6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	320.5	17.8	1137	4	US-09-107-532A-1088
2	305	17.0	1104	4	US-09-134-001C-841
3	253	14.1	5463	4	US-09-321-017B-610
4	216.5	12.0	4411529	3	US-09-103-840A-1
5	203.5	11.3	133206	4	US-08-961-527-33
6	191	10.6	1664976	4	US-08-916-421B-1
7	171.5	9.5	4403765	3	US-09-103-840A-2
8	106	5.9	771	4	US-09-252-991A-8080
9	106	5.9	888	4	US-09-252-991A-8235
10	104	5.8	789	4	US-09-328-352-356
11	101	5.6	3428	4	US-09-146-053-1
12	101	5.6	3428	4	US-10-002-593-9

13	100	5.6	1767	4	US-09-328-352-3868	Sequence 3868, App
14	97.5	5.4	969	4	US-09-252-991A-12362	Sequence 12362, A
15	97.5	5.4	1530	4	US-09-252-991A-12109	Sequence 12109, A
16	97.5	5.4	2091	4	US-09-252-991A-12312	Sequence 12312, A
17	94.5	5.3	1230025	4	US-09-198-452A-1	Sequence 1, Appl1
18	94	5.2	4215	4	US-09-620-312D-295	Sequence 295, App
19	92.5	5.1	8411	4	US-08-961-527-16	Sequence 16, Appl
20	92	5.1	2415	4	US-09-134-001C-2381	Sequence 2381, App
21	91.5	5.1	678	4	US-09-252-991A-12248	Sequence 12248, A
22	91.5	5.1	1219	4	US-08-936-165A-52	Sequence 52, Appl1
23	91.5	5.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
24	91	5.1	2208	4	US-09-134-001C-603	Sequence 603, App
25	91	5.1	1830121	4	US-09-557-884-1	Sequence 1, Appl1
26	91	5.1	1830121	4	US-09-557-884-1	Sequence 1, Appl1
27	91	5.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
28	91	5.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
29	90	5.0	1788	4	US-09-328-352-306	Sequence 306, App
30	90	5.0	3177	4	US-09-328-352-150	Sequence 150, App
31	89.5	5.0	2310	4	US-09-854-856-43	Sequence 43, Appl
32	89.5	5.0	2490	4	US-09-854-856-11	Sequence 11, Appl
33	89.5	5.0	2769	4	US-09-854-856-37	Sequence 37, Appl
34	89.5	5.0	2949	4	US-09-854-856-5	Sequence 5, Appl1
35	89.5	5.0	5820	4	US-09-854-856-47	Sequence 47, Appl
36	89.5	5.0	6000	4	US-09-854-856-15	Sequence 15, Appl
37	89.5	5.0	6099	4	US-09-854-856-41	Sequence 41, Appl
38	89.5	5.0	6231	4	US-09-854-856-45	Sequence 45, Appl
39	89.5	5.0	6279	4	US-09-854-856-9	Sequence 9, Appl1
40	89.5	5.0	6411	4	US-09-854-856-13	Sequence 13, Appl
41	89.5	5.0	6510	4	US-09-854-856-39	Sequence 39, Appl
42	89.5	5.0	6558	4	US-09-854-856-35	Sequence 35, Appl
43	89.5	5.0	6690	4	US-09-854-856-7	Sequence 7, Appl1
44	89.5	5.0	6738	4	US-09-854-856-3	Sequence 3, Appl1
45	89.5	5.0	6969	4	US-09-854-856-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1
US-09-107-532A-1088
; Sequence 1088, Application US/09107532A
; Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham,
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arliniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

```

; INFORMATION FOR SEQ ID NO: 1088:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 1137 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHEetical: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;       ORGANISM: Enterococcus faecium
;   FEATURE:
;       NAME/KEY: misc.feature
;       LOCATION: (B) LOCATION 1..1137
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1088:
US-09-107-532A-1088

Alignment Scores:
Pred. No.:      8,86e-30      Length:      1137
Score:          320.50        Matches:      100
Percent Similarity: 45.36%    Conservative: 81
Best Local Similarity: 25.06% Mismatches:    131
Query Match:    17.82%       Indels:        87
DB:             4            Gaps:         16

US-09-745-506-37 (1-350) x US-09-107-532A-1088 (1-1137)

OY      4  LysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTyrPasp 23
DB      31 CGCACCTTCATCCAAAAGCTTGAAGCTATTGTCCTCATGGCTAGCTGAAGCAAGACGAC 90
OY      24 AsnValGlyLeu-----LeuValGluProSerProProHisThrValAsnThr 39
DB      91 CCAAGTCGACATATGCGAAGCATTTGGATGACCA-----ATCCACAGA 135
OY      40 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluLysAla 59
DB      136 GTAATGATGACATTAAGACGTTGCTCCACAGAGTGGCGAAGAACATCAAGAAAAATC 195
OY      60 AspLeuLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTyrPasn 79
DB      196 GATTTCGATGTCGAACATCCCTCCATCTTTCCTCTGTAACAAAGCGCTGTTCTCAT 255
OY      80 ThrTyrLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerPro 99
DB      256 CAGCCACAGAAAGAAATGATATGATGTAACATGATATGCGCTATGCAACA 315
OY      100 HisThrAlaTyrAspAlaAlaProGluGluValAsnAsnTyrPheAlaLysGlyLeu 119
DB      316 CACACGAAACATGATATTATTTGGATGACGTAAGTGGTGTGTAACCTTCGCT 375
OY      120 -----AlaCysThrSerArgProIleHisProSerLysAlaProAsn 133
DB      376 ATTGAAAGTGAGAGATTATTAGTAAAGCATGATGATTCATTAAAAAACTGGCCGT 435
OY      134 TyrProThrGluGluAsnHisArgValGluPheAsnValAsnTyrThrGluAspLeuAsp 153
DB      436 TAT-----GTACCTGTGATCATGCACAGAAATGCGT 468
OY      154 LysValMetSerAlaValLysGly-----LleAspGlyValSerValThr 168
DB      469 GAAGATTAGTGCAGCTGTGTGTGTACACAAAGGTGATTATCCGGTACAAAGTTTACC 528
OY      169 SerPheSer-----AlaArgThr 174
DB      529 TCGATTGACACGCTGATTTACTCCGGAAGCTGTCACAAACGCAATGGGAAAGTA 588
OY      175 GlyAsnGluGluThrArgLysAsnLysAsnCysThrGluLysAlaLeuMetGluVal 194
DB      589 GGAAGACAGCAACA-----GTTCAAAGAGCAAAAGTTGAGGT 627
OY      195 ValAspPheLeuSerArgAsnLysGluLeuTyrGluLysThr----- 208

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DB      628 ATTTGCCGGAACATACGAAAAACAGTATTCACAGCATCGGTCATCTTAT 687
OY      209 -----GluIleLeuSerLeuGluLysProLeuLeuHisThrGlyMet 223
DB      688 GAGGAACCTGCTATTATGATCTTTGGCTATATACACAGTCGAAATGTT---GGGTGA 744
OY      224 GlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetLleAspArgLys 243
DB      745 GGACGAGTAGTGAATGCCCGCAAGAAATTTTATAGAGCATTTGTAGAACAAAGTAAA 804
OY      244 ArgHisLeuLysLeuSerHisLleArgLeuAlaLeuGluValGlyArgThrLeuGluSer 263
DB      805 GAACGCTTCACATGATGATGACATGAGTAATGATC-----CAGCCAAAAATGCAAAATCC 858
OY      264 GluValLysValAlaAlaLeuCysAlaGlySerGly-----SerSerVal 278
DB      859 TCTGTGAAGCCATTCGATTCGCGGTGGAAGCGGTGAATAATTTTATCCGACGACATC 918
OY      279 LeuGluGlyValGluAlaAspLeuTyrLeuThrGluGluMetSerHisAspThrLeu 298
DB      919 GCCCAA-----AGACGATGCTCATATCACGGAGATATCTATTATCATACGCTCAT 972
OY      299 AspAlaAlaSerGluGlyLleAsnValIle-----LeuCys 310
DB      973 GATATGCAAGCGCTGGGTGATTCATATCCCGGTCAATTATGTAATCGTTATGC 1032
OY      311 GluHisSerAsnThrGluArgGlyPheLeuSerAspLeuArgAspMetLeuAspSerHis 330
DB      1033 AAGCAGACATTTATTCGAGAAA---TTGCAATCTTGGAACAAAGAA----- 1074
OY      331 LeuGluAsn---LysIleAsnIleLeuSerGluThrAspArgAspProLeuGlu 348
DB      1075 --GAAATGTGGATATTAACCTTTCTGCTGTAACAAATACAAACCATTTCAA 1128

RESULT 2
US-09-134-001C-841
; Sequence 841, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;   TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC-007
;   CURRENT APPLICATION NUMBER: US/09/134,001C
;   PRIOR FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/064,964
;   PRIOR FILING DATE: 1997-11-08
;   PRIOR APPLICATION NUMBER: US 60/055,779
;   NUMBER OF SEQ ID NOS: 5674
;   SEQ ID NO 841
;   LENGTH: 1104
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-841

Alignment Scores:
Pred. No.:      7.06e-28      Length:      1104
Score:          305.00        Matches:      96
Percent Similarity: 43.54%    Conservative: 76
Best Local Similarity: 24.30% Mismatches:    145
Query Match:    16.95%       Indels:        78
DB:             4            Gaps:         13

US-09-745-506-37 (1-350) x US-09-134-001C-841 (1-1104)

OY      1  MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB      4  ATGAAATATAGTGAACGTATGAGAACTTTTAATAATATCAAGTTCATTCATCAACCTGAA 63
OY      21 SerTyrAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
DB      64  TCATGGATATATGATGATTTAATTT---GGTATGATTAAGTTAGATATTACAGGTAT 120

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Oy	41	PheleuThrasnaPleuThngluGluValMetGluIuValLeuGluIuLybalaasp	60
Db	121	STGCACAACTCGCTCGACCGAGATGTTGTATACCAAGCAATTTGAACCTTAATACCAAT	180
Oy	61	LeuIleLeuSerTyrHisProGluIlePheArgProMetLysArgIleThrTrpAsnThr	80
Db	181	ACCAATCTGTCATCATCTCACTATTGTTCAAGAGAAACGATACGTTGGAAGTTCGA	240
Oy	81	TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValAlaGlyIleTyrSerProHis	100
Db	241	TATGGTAGT---AATAATCGTAACTTAATCCAAATATATATACCAATCTTAATGCACTTAC	297
Oy	101	ThrIleTyrAspAlaAlaLeuProGluGlyValAlaAsnIlePheValIleLysGlyLeuGlyAla	120
Db	298	ACTAAATCTGTATGTAATATCCCTAAAGGGTGTCAATGCAATGTTAGGGAGATCAATAGT	357
Oy	121	CysThrSerArgProIleHisProSerLysAlaProAsnIleTyrProThr-----	136
Db	358	GAGAACATATACCAATGATTAATACAAATAGCCATATTAATACAAAGTTCAAACTTTTATA	417
Oy	137	-----Glu	137
Db	418	CCCTAAATATATATGTAAGATTTCAAAGACACGTTTAAACGAACCTTGATAGCTTAAGAA	477
Oy	138	GlyAsnHisArgValGluPhe-----AsnValAsnIleTyrThrGln	150
Db	478	GGTAAATATACGAATATGTTGTTCTTGAAAGTGAAGTAAAGGCAATTTGGACCGTAGCT	537
Oy	151	AspLeuAspLysValMetSerAlaValLysGlyIleAspGlyValSerValThrSerPhe	170
Db	538	GATCAACAGCTCTTATATATAGGAGAGCTTGATATGTAATGCTGAATATGTTGATAGATATAACT	597
Oy	171	SerAlaArgThrGlyAsnGluGluGlnThrArgIleAsnLeuAsnCysThrGlnLysAla	190
Db	598	GAGTTTATGATAAAGAACATGAA-----TTAGAAATACATCAACGCTCT	642
Oy	191	LeuMetGln-----ValValAspPheLeuSerArgAsnLysGln	203
Db	643	ATTTTATAGATAATCACCCATACGAACACCACTTTTGTATTTATTAATTAATACAAAGAA	702
Oy	204	LeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHisThrGlyMet	223
Db	703	-----AGCGATATGCGATTA	717
Oy	224	GlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIleLys	243
Db	718	GGGATTTTATGACACATTAATTAACCAACTATGACTTACATGTAATTTTGCATATAGCCAAA	777
Oy	244	ArgHisIleLeuLysLeuSerHisIleArgLeuAlaLeuGlyValAlaGlyArgThrLeuGluSer	263
Db	778	AAACAGCTCAATATACCGAGCGTACGAT-----ACAGGTCAACAT---GATAGT	825
Oy	264	GlnValLysValAlaAlaLeuCysAlaGlySerGlySerSerValIleGluGlyValGlu	283
Db	826	CCAAATTAGAAGAAAGTATCATATAGTGCGTTCAAGTATA-----GGATTTCAG	873
Oy	284	-----AlaAspLeuTyrLeuThrGlyGluMetSerHisHisAsp	296
Db	874	TATTAAGCTACCAACTGGACGAGATGTTTTGTTACTGCTGATATTAACACCATCATAT	933
Oy	297	ThrLeuAspAlaAlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAspThrGlu	316
Db	934	GCTTAGTAGCTTAATAATCCAAATGTAATTAATTAATGACATCAATCAT---TATGTAG	990
Oy	317	ArgGlyPheLeuSerAspLeuArgAspMetLysSerSerHisLeu-----GluAsn	333
Db	991	TATGTTATGAAGAAGAGATTAAAGAAATTAATGAAAAATGCTTATTTAAATAGAAAT	1050
Oy	334	LysIleAsnIleIleLeuSerGlyThrAspArgAspProLeuGln	346
Db	1051	CAATTTTCAATATATAGCTTCTGGAATCAACACAGATCCATTTTAA	1095

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US-09-221-017B-610
; Sequence 610, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 610:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5463 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...5463
; US-09-221-017B-610

Alignment Scores:
Pred. No.: 3,05e-20 Length: 5463
Score: 253.00 Matches: 94
Percent Similarity: 43.53% Conservative: 64
Best Local Similarity: 25.90% Mismatches: 128
Query Match: 14.06% Indels: 78
DB: 4 Gaps: 12

US-09-745-506-37 (1-350) x US-09-221-017B-610 (1-5463)
QY 1 MetaspleinysalileuleuseriserleuanaasphalaserleuserPhealagl 20
44 ATGATCATCTTCAGAGATATATAGAGGCTATCGAGCGGCTGCCCGGAGGCTTTCAGAGG 1030

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OY	21	SetThrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu	40
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Db	104	AGCTATACAAATAGTGGCTGCAGGTGGGCGACACCAAGCGGAGGACCAAGCGGTGCCCTC	163
OY	41	PhenLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluGlnLysLysAlaAsp	60
		:	:
Db	164	---CTGTGTGGATGTTTACCGAAGCGGTATTGGAGAGAGGCCAATGCCGTGGGATGCAT	220
OY	61	LeuIleLeuSerTyrHisProProPolePheArgProMetLysArgIleThrTrpAsnThr	80
		:	:
Db	221	CTGTCTCAATGCCCAACCAATCCGATCTTTTCAAAACCGCTCAAGAGATGGACCGGACAGCTCC	280
OY	81	TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis	100
		:	:
Db	281	TACGTGGAGGAGTGCSTGGAGAGCTGGCGGTACCGGACAGCTGTGGTGCATATTGGGGGTGAT	340
OY	101	ThrAlaTyrAspAlaAlaIaProGlnGlyValAlaAsnAsnTrpLeuAlaLysGlyLeuGlyAla	120
		:	:
Db	341	ACCAAATCGCGCAACAGCTCCGACAGGAGCTGAATGCCGTGGCGCGCAACCTTCGGCTGG	400
OY	121	CysThrSerArgProIleHisProSerLys-----AlaProAsnTyr	134
		:	:
Db	401	CTGAATACGCGACCGCTGGAGCGCCCTGCAGAGGCAAGCTCTTAAGACTGTCACCTTCGTC	460
OY	135	ProThrGluGlyAsnHisArgValGluIlePheAsnValAsnTyrThrGlnAspLeu-AspLys	154
		:	:
Db	461	CCCAAGCGGTATGCCGAGTGCCTGAGC-----CAGGGTCTGTGGCGAG	502
OY	154	sValMetSerAlaValLysGlyIleAspGlyValSerValThrSerPheSerAlaArgThr	174
		:	:
Db	503	GCCGGTGCAGGCGCTTTGGGGCATTTAGC---ATTGCTGTTCGTTCCACCAATGCCGCGACA	559
OY	174	rgLysAsnGluGlnThrArgIleAsnLeu-----AsnCysThr	187
		:	:
Db	560	GGGACTTTCAAGACTGCCAGCGGAGGCCCAATCCCTTTGGAGCGGATACAGCAATTGTGAC	619
OY	187	rgLlnLysAlaLeuMetGlnValValaPheLeuSerArgLysGlnLysGlnLeuTyrGlnLys	207
		:	:
Db	620	CATGAGGGGAGGAGAGCGGATCAGCTCGTACTGCCGC-----	656
OY	207	sThrGluLeuLeuSerLeuGlnLysProLeuLeuLeuHisThrGly-----MetGlu	224
		:	:
Db	657	-----CATACAGGAGGAGTACTGTGCTG	679
OY	224	YArgLeuCysThr-----LeuAspGluSerValSerLeuAlaHisMetIleAspArgIle	242
		:	:
Db	680	CAGGCTTTGGACCGCGGCTCATCCGTACAGAGCTGCCGGCTGTC-AGCCTGATCCGCGTGC	738
OY	242	eLysArgHisLeuLys-----	247
		:	:
Db	739	CAAGCATATCCCTCCGCGCGAGCGGCAATAGTGGGGATGTGCTTGCCCTTGCCCAATAAGGA	798
OY	248	-----LeuSerHisIleArgLeuAlaLeuGlyVal-----GlyArg	259
		:	:
Db	799	GCGGAGATGCTGCTGCACATCCAGAGAGATTCGGCTGTGAAGTCCSTGCCATTCGCGC	858
OY	259	gThrLeuGluSerGlnValLysValAlaIaLeuCysAlaGlySerGlySer-----	276
		:	:
Db	859	TTGGAGGGAGACGCGCTTGAGCGGATGGCTATATAGCGCGGCTAGCGGTGCTTTCATGTG	918
OY	277	-----SerValLeuGlnGlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHis	294
		:	:
Db	919	GCGCGCTGCAGACACAGAGGAT-----GCAAGACTTCTTCCGACAGGAGGAGCGGAAGTA	972
OY	294	sHisAspThrLeuAspAlaAlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAs	314
		:	:
Db	973	CACACACTTCTTCGTGCAGGGGAGACATGTGCTGTGTACAGATCGGTCAATTACAGAGAG	1032
OY	314	nThrGlu	316
		:	:
Db	1033	CGAAGAG	1039

```

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Alignment Scores:
Pred. No.: 9,236-11 Length: 4411529
Score: 216.50 Matches: 95
Percent Similarity: 44.01% Conservative: 63
Best Local Similarity: 26.46% Mismatches: 158
Query Match: 12.03% Indels: 43
DB: 3 Gaps: 15

US-09-745-506-37 (1-350) x US-09-103-840A-1 (1-4411529)
QY 19 AAGIUSERTPAPASNAVALGYLEULEUVALGLUBROSERPROPHOIHSTRHVALASN 38
DB 2504546 GCCCAGTGTGGGATCGGTGGG-----CTGTGTGCGCGGACACCCGACGACGAGTGTGGAT 2504490
QY 39 Thrleupheleuthrhnasplleuthrclugluvalmetclugluvalleuglnlysls 58
DB 2504489 TCGGTGACCGTGGCGGTGGACGCGACCGCGCGGTGGGACGACGTGCCAG----- 2504436
QY 59 AAlasplleulleuserTyrHisproproilephearPrometltsArgliethrtp 78
DB 2504435 GCCGACGTGATTTGGTGCCACACCCGTTGTTACTGCGTGGGGTCAATAGGTGCGGCC 2504376
QY 79 AasnhrtrplysGLUARGLEUVALILEARGALALEUGLUNSNARGVALIGLYIETYSER 98
DB 2504375 AACACGCCAAGGCGTGTGTGTGGACCGCTGATCCGACCGGTGCTGTTGTATACC 2504316
QY 99 ProIHSTRHVALTYRASPLAALAPROGLINLYVALASNASTRHPLAVALALYSGLYLEU 118
DB 2504315 GCCGACACCAACGCCGACCTGGCGGCGGTGTGTGCCAGCGGTGGCACACGCTGTT 2504256
QY 119 GLYALACYSthrsrArgProileHISProserLYSAlAPROASN----- 133
DB 2504255 GGTCTGACCGGTGACGCCGCTTGTGACCCG-----GTGCCGGAAGGGCGCGATCTGCAC 2504202
QY 134 -----TyrProthrglUGLYASNHSARGVAL-----Glu 143
DB 2504201 AAGTGGGTCATCTATGTGCGCGGACAGAACTACAGAGCGCGCGGACAGCGTCTTGAG 2504142
QY 144 pheasnVALsnrTYrThglnaspleuasplysVALmetserAlaVALylsGlyILE--- 162
DB 2504141 GCCGGTGGCGGCAATACGGCGCACACTACGACCTGCAAGTGTGGCGGTACCGGG 2504082
QY 163 -----AspGLYALSERVALHrserPheSerAlaArgThgLYASNGLU 177
DB 2504081 CAGTTCCTGGCGCACAGCGGGGCGTGGCGCCGATAGCAGACGTCGATACCGTGAACGG 2504022
QY 178 ---GluGlnThrArgIleASNleuSNcysThrGlnTASALeumetGlnVALVALASP 196
DB 2504021 GTGGCGGAGACCGGGGTCAAGTGTCTCCACCCGACACAGCGCGCGCGGACGAGTGTGGCG 2503962

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OY	197	cheuSerAArgAnuLysGlnLeuThrGlnLysThr-----GluLeuSerLeuGlu	214
		::: ::: ::: ::: ::: ::: ::: :::	
Db	2503961	GGCAGT---GGCGCGCGGACCCCTTACAGAGAGCGCGCATTCGCATCTTCGGCCGTGA	2503905
OY	215	LysProLeuLeuLeuLeuHisThrGlyMetCylValArgLeuCysThrLeuAspGlnSerValSer	234
		::: ::: ::: ::: ::: ::: :::	
Db	2503904	CCACCG---CCGGCGGCGACAGCGGGTGGACGGGATTTGGACAGATCGCAAAACCGGACCG	2503848
OY	235	LeuAlaThrMetIleAspArgIleValArgHisIleuLysLeuSerHisIleArgLeuAla	254
		::: ::: ::: ::: ::: :::	
Db	2503847	CTGGCGCACCTTTGTGGCCCGGTGTGAGCGCGGTGGCGCGACT-----GCG	2503800
OY	255	LeuGlyValAlaGlyArgThrLeuGlnSerGlnValLysVal-----ValAlaLeuCysAla	272
		::: ::: ::: ::: ::: ::: :::	
Db	2503799	ACCGGTGTGGCGCGCGCGGGAGATCCGACCTCGTGtGtGCGGGTGGCGGTGGCGGCG	2503740
OY	273	GlySerGlyLysSerSerValLeuGlnGlyValGluAla-----AspLeuTyrLeuThr	289
		::: ::: ::: ::: ::: ::: :::	
Db	2503739	GGCGCCGGGGGCTCTGGTGTTCGGCCACCGCTGGCGCGCGCGAGCATGAAGGTATGATACG	2503680
OY	290	GlyIleuMetSerHisHis-----AspThrLeuAspAlaIleSerGlnGlyIleAsnVal	307
		::: ::: ::: ::: ::: ::: ::: :::	
Db	2503679	GGCGATCTGGCAGCATCATCCAGCGGACGAGCATTTGCCGAGCTTGGCAA---GTGGCCCTG	2503623
OY	308	IleLeuCysGlnIleHisSerAsnThrGluArgGlyPheLeuSerAspLeuArgAspMetLeu	327
		::: ::: ::: ::: ::: :::	
Db	2503622	ATCACACGTCCGGCATTTGGGCAAGCGAATTCCTCCGTGTGGCGGACGCGCGCAAGATGTGG	2503563
OY	328	AspSerHisLeuGlnAlaAnuLysIleAsnIleIleLeuSerGluThrAspArgAspPro	346
		::: ::: ::: ::: ::: ::: :::	
Db	2503562	CGGTCGTATTTGGCGCGGTGGCTCGGCTGGGTGTGTGACACCATCTGCACCGACCGACCG	2503506

Db 10793 GATGGTTCCTGCTGATTCGACCCAGGTCAC---TATATCCAGATGATTTTGTGAAAAA 10737
QY 323 leuAtrgspwleuAtrgspwleuAtrgspwleuAtrgspwleuAtrgspwleuAtrgspwleu 339
Db 10736 ATCCGACAGCTTCTTGTGATGATGAGAGATTAAGGGGTGCTGATGATGATCTTGCT 10677
QY 340 SerGluhrasparGaspPC 346
Db 10676 AGTCAGCATCCACCAATCC 10656
RESULT 6
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
coccus jannaschii
Patent No. 6503729
FILE REFERENCE: P8275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature

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NAME/KEY: misc.feature
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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Alignment Scores:
Pred. No.: 2.56e-08 Length: 1664976
Score: 191.00 Matches: 70
Percent Similarity: 38.218 Conservative: 58
Best Local Similarity: 20.908 Mismatches: 111
Query Match: 10.628 Indels: 96
DB: 4 Gaps: 8

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US-09-745-506-37 (1-350) x US-08-916-421B-1 (1-1664976)

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OY 1 MetAspLeuAlaLeuSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB 614963 ATGAAGCTAAAGAGCTTATTAAGTTAAACCTTTCCTTAAGATTGGCTAAT 615022
OY 21 SerTrpAspAsnValGlyLeuValGluProSerProHisThrValAsnThrLeu 40
DB 615023 GAGGAGATTAACATTGGCTTCAAGTTGACACACCTTGTGATTAAGATAAAGCTA 615082
OY 41 PheLeuAsnAspLeuThrGluValMetGluValLeuGlnIleValAsp 60
DB 615083 GGTAAATGCTTAGACCTTCATTATTAAGCTTAATAAAGAGAGAGATTAAT 615142
OY 61 LeuIleLeuSerTyHisProIlePheArgProMetLeuArgIleThrTrpAsnThr 80
DB 615143 TTTTATTTTAAACCATCACTTATTAAGACCCCTATTAAGAAATTTTACTGGAGTTAAT 615202
OY 81 TrpValGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleValSerProHis 100
DB 615203 TACAAAAAATAAAGATTAATTA-----ATGAAATAATGATCATCTCTACTCTGCTCAT 615256

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OY 101 ThrAlaTyrAspAlaIleProGlnGlyValAsnAsnTrpLeuAlaIleGlyLeuGlyAla 120
DB 615257 ACAAAATTAGATATATGCAAAAATGGCTGATGATGATGCTTTAGCTGATTAATTAATTA 615316
OY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyProThrGluGlnAsnHis 140
DB 615317 GAAATCCAAAGCCCTTA----- 615334
OY 141 ArgValGluPheAsnValAsnTyThrGlnAspLeuAspLysValMetSerAlaValLys 160
DB 615335 -----TATGATTAATGCACTTGAAGACTT----- 615358
OY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrClyAsnGluGlnIleThr 180
DB 615359 -----GGAATTTTAAAGAACTTTTGA----- 615382
OY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSerArg 200
DB 615383 -----GAAATTTTGGAGATA 615397
OY 201 AsnLysGlnLeuTyGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
DB 615398 ACTAAAAAATACATTCACAAAAACCTATTTGTTTAAAGTAA----- 615442
OY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
DB 615443 -----GAGTATGATGACAACTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 615475
OY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
DB 615476 -----TCTGTTATGATGATGATGCT 615493
OY 261 LeuGluSerGlnValLysValAlaLeuCysAlaGlySerClySerSerValLeuGln 280
DB 615494 ---CAATCATCCCTAAAGATGATGCT----- 615517
OY 281 GlyValGluAlaAspLeuTyLeuThrGlyGluMetSerHisAspThrLeuAspAla 300
DB 615518 ---GAGAAAGCAGATGCTATCTTCTGGAGATTAACATCACTTCAAAATTTAAGCT 615574
OY 301 AlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrLysGlyPheLeu 320
DB 615575 GAGGACCTTGCTTACTGTTGTGTGATGCTACTACTACTCACTCAAGTTTGGATTA 615634
OY 321 SerAspLeuAspMetLeuAspSerHisLeuGlnAsnLysIle 335
DB 615635 AAGAAATTTAAAGATTCTTATCTTCAAAATTAAGATTTAAGAAATA 615679

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RESULT 7

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US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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Alignment Scores:

Pred. No.: 3,53e-05 Length: 4403765
 Score: 171.50 Matches: 97
 Percent Similarity: 43.32% Conservative: 65
 Best Local Similarity: 25.40% Mismatches: 140
 Query Match: 9.53% Indels: 74
 DB: 3 Gaps: 13

US-09-745-506-37 (1-350) x US-09-103-840A-2 (1-4403765)

QY 19 AlagLuserTrrpAraPnaValGlyLeuLeuValGluProSerProHsthrValAsn 38
 DB 2501787 GCCAGTCTGCTGGGATTCGGTGGT---CTGGTGTGGCGGACCCGACGACGCTGTGGAT 2501731
 39 ThrLeuHeuLeuTrrpAraPnaLeuThrgLugluValMetGluGluValLeuGluLys 58
 DB 2501730 TCGGTGACCGCTGGGGGTGGAGCGACCGCGGGGTGGTGACGATACGTTCCCGAG----- 2501677
 59 AlaAspLeuLeuLeuSerTrrpHisProProIlePheArgProMetLysArgLleThrTrp 78
 DB 2501676 GCCGAGCTGCTATGTGCACACCCGTTGTACTGCGTGGGGTGCATACGATACGCGGCC 2501617
 79 AsnThrTrpLysGluArgLeuValLleArgAlaLeuGluAsnArgValGlyLleTyrSer 98
 DB 2501616 AACACGCCAAGGGGTGTGCTGTGCACCGCTGATCCGACCGGTGCTGCTGTTCAC 2501557
 99 ProHsthrAlaTrrpAspAlaAlaProGluGlyValAsnAsnTrrpLeuAlaLysGlyLeu 118
 DB 2501556 GCGACACCAACGCGGACTGCGCGGTGCGGGGTGTGTGCAGCGCGCTGGCACGCTTT 2501497
 119 GlyAlaCysTrrpSerArgProIleHisProSerLysAlaProAsnTrrpProThrgLugly 138
 DB 2501496 GGTCTGACCGTGCAGCGCGCTGTCTGCACCG----- 2501467
 139 AsnHisArgValGluPheAsnValAsnTrrpThrgLusPheAspLysValMetSerAla 158
 DB 2501466 -----GTGCGCGGACCGCGCATCTGCACACATGGGTCTCATCTAT 2501428
 159 Val-----LysGlyLleAspGlyValSerValThrSerPheSerAlaArgThrgLysAsn 176
 DB 2501427 GTGCGCGCGGACGACTGAGAGCGGGTGGCGGAGCGGTCTTGTAGCGCGCGGCAT 2501368
 177 -GluGluGlnThrArg-LleAsnLeuAsnCysTrrp--GluLysAlaLeuMetGluVal 195
 DB 2501367 ATCGGCGACTACTGCTGACGCTGAGTGTGCGGGTACCGAGTCTCTCTGCGCAC 2501308
 195 AlaPheLeuSerArgAsnLysGln--LeuTyrGlnLysThr----- 208
 DB 2501307 GACGGGGGCTGCGCGCATAGCAGCGTCCGTACGTCGACGAGGGTGGCGGAGACCGG 2501248
 208 ----- 208
 DB 2501247 GTGAGGTCTGTCGACCGCGACGAGCGCGCGCGAGGTGGGGCATGCGCGCGCGC 2501188
 209 -----GluLleLeuSerLeuGluLysProLeuLeuLeuHst 221
 DB 2501187 ACCCTTACGAGAGCGCGCATCTTCGCTGCGCTGATACACCG--CCGGTGGCA 2501131
 221 hngLysMetGlyArgLeuSerTrrpHisPheAspGluSerValSerLeuAlaThrmLleAspA 241
 DB 2501130 GCGGGTTAGCGCGGATTCGACAGACTGCC-AAAAACCGAACCCTGCGACTTGTGGCC 2501072
 241 rGileLysArgHisLysLeuSerHisLleArgLeuAlaLeuGlyValGlyArgThrL 261
 DB 2501071 GTCTGAGAGCGCGCTGGCGCGCGACT-----GCGACCGGTGTGGCGCGCGCGC 2501024
 261 euGluSerGluValLysVal-----ValAlaLeuCysAlaGlySerGlySerValL 279
 DB 2501023 GGGATCCCGACCTGCTGGTGTGCGGGTGTGCGC-GGCGCGGGGACTGCTGGTC 2500965
 279 euGlnGlyValGluAla-----AspLeuTyrLeuThrgLuglyMetSerHisHis- 295

DB 2500964 TTGCCACCGTGGCGCGCGGACGCTGCACAGCTACTTACGGCGCATCTGCACATCATC 2500905
 QY 296 ----AspThrLeuAspAlaLaseGlnGlyLleAsnValLleLeuCysGluHisSerA 314
 DB 2500904 CAGCCGACGAGCATTTGCCGACTTCGCA--GTGGCCCTGATCGACGTCGCGCATGGG 2500848
 QY 314 snThrgLUAArgGlyPheLeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnL 334
 DB 2500847 CAACGGAATTCCTCGTGTGGCGCGGACGCGCGGAAAGTGTGCGTCTCATTTGCGCGCT 2500788
 QY 334 yLleAsnLleLleLeuSerGluThrAspArgAspPro 346
 DB 2500787 CGCTGCGCGTGGCTGTGTGCACCATTCGACCGACCGC 2500750
 RESULT 8
 US-09-252-991A-8080
 ; Sequence 8080, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8080
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8080
 Alignment Scores:
 Pred. No.: 0.0019 Length: 771
 Score: 106.00 Matches: 63
 Percent Similarity: 31.31% Conservative: 40
 Best Local Similarity: 19.15% Mismatches: 124
 Query Match: 5.89% Indels: 102
 DB: 4 Gaps: 9

US-09-745-506-37 (1-350) x US-09-252-991A-8080 (1-771)
 QY 3 LeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrp 22
 DB 25 CTGACACCGCTGTGAGAGAGCGCGACCGTATATCGATGCGCGCGCATCCAGAGACTAC 84
 QY 23 AspaAsnValGlyLeuLeuValGluProSerProHsthrValAsnThrLeuPheLeu 42
 DB 85 TGCCCGAAGCGCTCAGGTGCGAAGCGCGCG-----CAGTCCGCGGATCTGCAGC 138
 43 ThrAsnAspLeuThrgLugluValMetGluGluValLeuGlnLysLysAlaAspLeuLle 62
 QY 139 GGGGTACTGCCGACGACGCGCTGCTGATGCGCGCGGTGAGGCGGACGCGACGCTGGT 198
 DB 63 LeuSerTrrpHisProProIlePheArgProMetLysArgLleThrTrpAsnThrTrpLys 82
 QY 199 CTGGTGCATCAGCGTACTTCTGGAAGGTGAGAACCCCTGGTGGTGGC--ATGAAG 255
 DB 83 GluArgLeuValLleArgAlaLeuGluAsnArgValGlyLleTyrSerProHsthrAla 102
 QY 256 CAACGCGCTGTAACACCTGCTGTAACACGATATACCTGCTGCTTACACACCTGGCG 315
 DB 103 TyrAspAlaAlaProGln--GlyValAsnAsnTrrpLeuAlaLysGlyLeuGlyAlaCys 121
 QY 316 CTGATCTGCATCCGAGGTGGGCAACAACGTCGACGCTGCGCGGACGCTGGCTTCGAA 375
 DB 122 ThrSerArgProIleHisProSerLysAlaProAsnTrrpProThrgLuglyAsnHisArg 141
 QY 376 GTGGAAGGCGCTGTGAGCGC-----GGCAACCGCGGT 408


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Oy 142 ValGluPhaGlnValAsnValThrGlnAspLeuAspLysValMetSerAlaValLysGly 161
Db 408 ----- 408
Oy 162 IleAspLysValSerValThrSerPheSerAlaArgThrGlyAsnGlnGlnThrArg 181
Db 409 -----TCC 411
Oy 182 IleAsnLeuAsnCysThrGlnLysAlaLeuGlnValAlaAspPheLeuSerAlaGln 201
Db 412 ATGCTCCCTCCGTTGGTGGCTGGCCGAGCCGATGAGCTTCGATTCGCTCGCATGTG 471
Oy 202 LysGlnLeuValThrGlnLysIleLeuSerLeuGlnLysProLeuLeuAsnIsthr 221
Db 472 CGCGATCGCGTGGGGCGCT-----GAGCGCGCTGTCGTGATGCC 510
Oy 222 GlyMetLysArgLeuCysThrLeuAspLysValSerLeuAlaThrMetIleAspArg 241
Db 511 GGT----- 513
Oy 242 IleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeu 261
Db 513 ----- 513
Oy 262 GluSerGlnValLysValAlaLeuCysAlaGlySerGlySerValLeu--Gln 280
Db 514 ---CAGCCGATCCCGGCGCATCGCTGGTGCACCGCGCGCCAGGCGCTATATCGACAG 570
Oy 281 GlyLysAlaLys-----AspLeuTyrLeuThrGlyLysMetSerHisIsthrAspThrLeu 298
Db 571 GCGATCGCGCTGGCGCTGATGCTGCTACCTACCGCGGCGATTCCTCGAGCAGACCGTGCAC 630
Oy 299 AspAlaAlaSerGlnGlyIleAsnValIleLeuGlnLysIsthrSerAsnThrGlyArgGly 318
Db 631 AGCCGCGGAGAACGCGCATCAGCTTCATCGCCCGCGACACCATGCCACGAGCGCTAC 690
Oy 319 PheLeuSerAspLeuArgAspMetLeu 327
Db 691 GGGGTACAGCGCTTGGCGCACTACTGTG 717

RESULT 9
US-09-252-991A-8235/c
Sequence 8235, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8235
LENGTH: 888
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8235

Alignment Scores:
Pred. No.: 0.00241 Length: 888
Score: 106.00 Matches: 63
Percent Similarity: 31.31% Conservative: 40
Best Local Similarity: 19.15% Mismatches: 124
Query Match: 5.89% Indels: 102
DB: 4 Gaps: 9

US-09-745-506-37 (1-350) x US-09-252-991A-8235 (1-888)

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QY      3 LeuysAlaIleuSerSerIleuAsnAspRheAlaSerLeuSerPheAlaGluSerTrp 22
      ||| |||.....:.....:.....:.....:
Db      834 CTGACACCCTGTGGTCAGACAGCCGCGTTATCTGATGCCGGCGCATCCAGACTAC 775
      ||| |||.....:.....:.....:
QY      23 AspAsnValAGlyLeuLeuValGluProSerProPronHisThrValAsnThrPheLeu 42
      ||||| ||||| ||| ||| ||| |||
Db      774 TGCCCGAAGCGCTCGAGTCCAGTACAGCCGCGCC-----CAGTGGCGGAGATCGTCAC 721
      ||| |||.....:.....:.....:
QY      43 ThrAsnAspRheTrhGluGluValMetGluGluValLeuGluIleValAspLeuIle 62
      :|||: :|||: :|||: :|||: :|||: :|||:
Db      720 GGGGTCACTGCCACGACGCGCTGCTGATGCCGCGCTGAGAGCCGACCCGACGTCGTG 661
      :|||: :|||: :|||: :|||: :|||: :|||:
QY      63 LeuSerTrpHisProProIlePheAsnArgPrometLysArgIleThrTrpAsnThrTrpLys 82
      ||| |||.....:.....:.....:
Db      660 CTGGTGCATACACGGTACTTCTTGAGAGGGTGAAGAACCCCTGCTGCTCGCG--ATGAG 604
      ||| |||.....:.....:.....:
QY      83 GluArgLeuValIleArgAlaLeuGluAsnArgValAGlyIleTrpSerProHisThrAla 102
      :|||: :|||: :|||: :|||: :|||: :|||:
Db      603 CACAGCGCGCTGACAGCCCTGCTGACAAACAGATACGATCTGCTGCTTACACACGCGCG 544
      :|||: :|||: :|||: :|||: :|||: :|||:
QY      103 TyrAspAlaAlaProGln--GlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCys 121
      ||| |||.....:.....:.....:
Db      543 CTGGATCTGCATCCGAGGCTGGGCAACAGCTGCACCTGCGCGGACGCTCGGCTTCGAA 484
      ||| |||.....:.....:.....:
QY      122 ThrSerArgProIleHisProSerLeuysAlaProAsnTrpProThrGluGluHisAsp 141
      ||| |||.....:.....:.....:
Db      483 GTGAGAGCGCGCTGTGAGCCG-----GCCAACCCGCGT 451
      ||| |||.....:.....:.....:
QY      142 ValGluPheAsnValAsnTrpThrGlnAspRheAspLysValMetSerAlaValLysGly 161
      ||| |||.....:.....:.....:
Db      451 ----- 451
      ||| |||.....:.....:.....:
QY      162 IleAspGlyValSerValThrSerPheSerAlaAspThrGlyAsnGluGlnThrArg 181
      ||| |||.....:.....:.....:
Db      450 -----TCC 448
      ||| |||.....:.....:.....:
QY      182 IleAsnLeuAsnCysThrGlnIleuysAlaLeuMetGlnValAlaAspPheLeuSerAlaAsn 200
      ||| |||.....:.....:.....:
Db      447 ATCGTCTCTCTCGTGGTCCGTTGCCGAGCCGATACGCTGCCGATTTCCGTCGGCATGTG 388
      ||| |||.....:.....:.....:
QY      202 LysGlnLeuTrpGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHisThr 221
      :||: :||: :||: :||: :||: :||:
Db      387 CGCGATCGCGCTGGGCGCT-----GACGCGTGCCTGCGTCATGCC 349
      ||| |||.....:.....:.....:
QY      222 GlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArg 241
      ||| |||.....:.....:.....:
Db      348 GGT----- 346
      ||| |||.....:.....:.....:
QY      242 IleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyAlaGlyThrLeu 261
      ||| |||.....:.....:.....:
Db      346 ----- 346
      ||| |||.....:.....:.....:
QY      262 GluSerGlnValLysValAlaAlaLeuCysAlaGlySerClySerSerValLeu---Gln 280
      :|||: :|||: :|||: :|||: :|||: :|||:
Db      345 ---CACCCGATCCGGGGCATCCGCTGCTGTCACCGGGGGCCCAAGGGCTATATCAGACAG 289
      :|||: :|||: :|||: :|||: :|||: :|||:
QY      281 GlyValAGluAla-----AspLeuTrpLeuThrGlyGluMetSerHisAspThrLeu 298
      :||: :||: :||: :||: :||: :||:
Db      288 GCGATCGCGCTGGCGCTGATGCTGCTACCTGACCGGAGGAGTTTCCAGACGACAGCCGTGAC 229
      :||: :||: :||: :||: :||: :||:
QY      299 AspAlaAlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgGly 318
      ||| |||.....:.....:.....:
Db      228 AGCGGCGCGGAGACAGCGCATTCACGTCATCGCGCCGACACCATCCACCGAGCGCTAC 169
      ||| |||.....:.....:.....:
QY      319 PheLeuSerAspLeuArgAspMetLeu 327
      ||| |||.....:.....:.....:
Db      168 GGGGTACAGCGCTTGCGGCTACTACCTG 142
      ||| |||.....:.....:.....:

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: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 356
: LENGTH: 789
: TYPE: DNA
: ORGANISM: Acinetobacter baumannii
: US-09-328-352-356

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Alignment Scores:	
Pred. No.:	0.00349
Score:	104.00
Percent Similarity:	31.22%
Best local Similarity:	19.06%
Query Match:	5.78%
DB:	4
Length:	789
Matches:	69
Conservative:	44
Mismatches:	112
Indels:	137
Gaps:	14

US-09-745-506-37 (1-350) x US-09-328-352-356 (1-789)

Oy	6	LeuIeuSerSerLeuAsnAspPheAlaIleSerIleSerPheAlaGluSerTrp---	AspAsn 24
		:::	
Db	10	CTACTCAATTCAAGAAATATCATCGCAAAATTTCATGAAATTATTCAGTGGCGCA	69
Oy	25	Val-----	GlyLeuLeuValGluProSer 32
Db	70	ACCTTAAAGCAGCAATTTTAAAGATTACGCACCAAAATGGCTCGAATTAAGGTCA	129
Oy	33	ProProHISThrValAsnThrLeuPheLeuThrAsnAspLeuThrGluLeuValMetGlu	52
Db	130	ACT-----GAAGTAAACGTAATTTCTTGTGCGAGTAACCTGCTTCGAATGCAATGTAT	183
		:::	
Oy	53	GluValLeuGlnLysLysAlaAspLeuIleLeuSerTrpHisProProIlePheArg----	71
		:::	
Db	184	GCAGCGAATTGCCTAAGAAATGCTGATCTCTTACGTCGACACCGAGTATTTTGGAAAGC	243
Oy	72	-----PrometLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArg	88
Db	244	GAACCGTATTCCAATTACGTGATGCGAGGTAAACCGTATAA-----	288
		:::	
Oy	89	AlaIleuGluAsnArgValGlyIleLeuSerProHISThrAlaTrpAlaIleProGln	108
Db	289	CTTATTCAAAATAATATCATCATAGCTGCTACCACTGCGCTTAAATGACATCCGAGT	348
		:::	
Oy	109	---GlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIle---	126
		:::	
Db	349	TTAGCGCAATTAATATGCGCTATTCGACAAAACCTAACTCAAAATTTAGAACCACTTGAT	408
Oy	127	-----HisProSerLysAlaProAsnTrpProThrGluGlnLysHISArgVal	142
Db	409	CTAACTGAGAAACATCCAAATGGT-----	432
Oy	143	GluPheAsnValAsnTrpThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle	162
Db	433	-----AATATCGGTTATTATTAAG-----	450
		:::	
Oy	163	AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIle	182
Db	451	CAAGCGCTTTCGTGAGAGCAATTTAAACGAAAA-----	483
Oy	183	AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLys	202
Db	484	-----CTACCAAAACGGTTTGTGATTT-----	507
Oy	203	GlnLeuTrpArgLysThrGlnIleLeuSerLeuGluLysProLeuLeuHISThrGly	222
Db	508	GTGATCCATTTACCGCGTGAAAAACAAAGATTCAAAA-----	546
Oy	223	MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle	242

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Db      546 ----- 546
Oy      243 LysArgHisLeuLysLeuSerHisLeuArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
Db      546 ----- 546
Oy      263 SerGlnValLysValAlaLeuGlyValGlySer-----GlySer 277
Db      547 ----- 547
Oy      278 ValLeuGlnGlyValGlyAlaAlaSerLeuArgThrGlyGluMetSerHisAspThr 297
Db      592 GCTTACAA-----AATTGCATGCTTATATTTCAGCGCAGTCAAGTCAAGCAACTTTT 645
Oy      298 LeuAspAlaAlaSerGlnGlyLeuAsnValIleLeuGlyGlnHisSerAsnThrGluArg 317
Db      646 TATGACGCAAAAGAAATTAAGCGCTTATATTTTGGCTGTGGCCATGCAACCGAAGT 705
Oy      318 GlyPheLeuSerAspLeuArgAspMetLeu-AspSerHisLeuGluAsnLysIleAsnI 337
Db      706 TATGGGGTTCACACGTTTACGACACAGCAATTTCAAAACAGTTTGCATTGTAAGTGAATAT 765
Oy      337 eile 338
Db      766 TTTG 769

RESULT 11
US-09-146-053-1
; Sequence 1, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146, 053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057, 854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3428
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (265)..(2283)
; US-09-146-053-1

```

Alignment Scores:		
Pred. No.:	0.1	Length: 3428
Score:	101.00	Matches: 69
Percent Similarity:	35.33%	Conservative: 55
Best Local Similarity:	19.66%	Mismatches: 123
Query Match:	5.61%	Indels: 104
DB:	4	Gaps: 15

US-09-745-506-37 (1-350)	x	US-09-146-053-1 (1-3428)
QY	20	GIUSERTPASPASNAVALGYLEULeuValGILPProSerProRHSThrValAsnThr 39
DB	754	GACACCTGGAGAGGTTATGATCTCGGCCCTCCAGAGCTTACACAGACAGCGTGGTCC-- 810
QY	40	LeupheLeuThrAsnAspLeuThrGIUGluValMetGluGluValLeuGlnLysAla 59
DB	811	ATCACAAACCAATCTTGTGGAGCTGTGATGGGGA-- 843
QY	60	AspLeuLeuLeuSerThrHisPro-----ProIlePheArgProMetLys 74
DB	844	-----TCAAGAGAGCCACCGGTTCCAAATCAACCACTTATGCGCCCTGCAGAG 891

QY 75 ArgIleThrPaspnThrTrpIysGluArgLeuValIleArgIleLeuGluAsnArgVal 94
Db 892 GCATTACAGAGGAGCACTTGGCAGGAGAAAGTA-----TCG 927
QY 95 GlyIleTyrSerProHisThrAlaTyrAspAlaIleProGlnIlyVal-----110
Db 928 GGCCTCCGAGAGCAGATCCAGAGCAAAAGTCCGACCTGCTCTGTGTGGCG 987
QY 111 -----AsnAsnTrpLeuAlaIlysgIlyLeuGlyAlaCysThrSerArgProIleHis 127
Db 988 CTTCGAGAGAGCGGCTGGCTTTCAAC-----CTTCGA 1020
QY 128 ProSerIlyAspAlaProAsnTyrProThrGluGlyAsnHisArgValGluPheAsnValAsn 147
Db 1021 GCCAGTGCATCCCTCAATAACCC-----TTCTCTATATCC 1056
QY 148 TyrThrGlnAspLeuAspIlyValIleMetSerAlaValIlysgIlyLeuAspIlyValSerVal 167
Db 1057 TACACGCTGCTGCACAGAC-----TCTTCTATATAGGTTG 1089
QY 168 ThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIleAsnLeuAsnCysThr 187
Db 1090 TTTCGAAACAGAGAGTGGCTTTAGCTCCGAAACCTTGAGCTATGAACTTCAGTTGCACA 1149
QY 188 GlnIlyAspAlaLeuMetGlnValValAspPhe-----197
Db 1150 GGGCCCATGTGTGCAAAATCGAGATTACAGCCAAATTGCTGCACAGCATCCAGGCTAC 1209
QY 198 -----LeuSerArgAsnIlysgIleuTyrGlnIlyThrGlu 209
Db 1210 TCATTGGAGATGTGAGAGATCTGGATTGGACACCATATACCATGTATGCGATCTATGAA 1269
QY 210 IleLeuSerLeuGluIlyProLeuLeuHisThrGlyMetGlyArgLeuCysThrIleu 229
Db 1270 ATGATACCAAGGAGAGAA-----CTCGTG 1293
QY 230 AspGluSerValSerLeuAlaThrMetIleAspArgIleAspArgHis-----245
Db 1294 ACAGACACCTACTCCCGAGATGATGACCAAGCAAGCAAGCAAGCAAGCAAGCC 1353
QY 246 ---LeuIlyLeuSerHisIleArgIleAlaLeuGlyValGlyArg-----ThrLeu 261
Db 1354 CTCCTCAAGCCCGCCGAGCGTGGCGAGCTGTGCTGATCCGATCTGTGCTGCTG 1413
QY 262 GluSerGlnValIlyValIlyAlaLeuCysAlaGlySerGlySerSerValIleuGlnIly 281
Db 1414 GAGAGACAGCTGCCAAAGCAGACAGATGAGATTTTCGGGGCAGAGATCGTGACAG 1473
QY 282 ValGluAlaAspLeuTyrIleuThrGlyGluMetSerHisThrIleuAspAlaIle 301
Db 1474 TTCGAGAGAGAGACAGATTCCTCCGAGCCAGT---TTTGAACCATCTCTGCTAGT 1530
QY 302 SerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGlu-----ArgGly 318
Db 1531 ---GGTTTGAATCTGCTCCCGCCCACTACAGCCCGCAGAGAGTGAAGCCGCAAG 1584
QY 319 PheLeuSerAspLeuArgAspMetLeuAspSer 329
Db 1585 CTGTCTCTCAATGAGATGTAACCTGTGCTGACTCT 1617

RESULT 12
US-10-002-593-9
; Sequence 9, Application US/10002593
; Patent No. 6586198
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIN
; TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
; FILE REFERENCE: Atty Docket No. 6586198 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; PRIOR APPLICATION NUMBER: 60/244,524

; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 3428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-002-593-9

Alignment Scores:
Pred. No.: 0.1 Length: 3428
Score: 101.00 Matches: 69
Percent Similarity: 35.33% Conservative: 55
Best Local Similarity: 19.66% Mismatches: 123
Query Match: 5.61% Indels: 104
Gaps: 15

US-09-745-506-37 (1-350) x US-10-002-593-9 (1-3428)

QY 20 GluSerTrpAspAsnValGlyLeuValIleProSerProHisThrValAsnThr 39
Db 754 GACACCTGGAGAGATTATGATCTGGCCCTCAAGCTCTAAGACAGCTGTGCTCC---810
QY 40 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValIleuGlnIlyAspAla 59
Db 811 ---ATCACACCAATCTGTGACCTGTGAGGA-----843
QY 60 AspLeuIleLeuSerTyrHisPro-----ProIlePheArgPrometIly 74
Db 844 ---TCAGAGAGCCACCGCTTCCAAATCAACCATTTATATGCCCTGCAGAG 891
QY 75 ArgIleThrPaspnThrTrpIysGluArgLeuValIleArgIleLeuGluAsnArgVal 94
Db 892 GCATTACAGAGGAGCACTTGGCAGGAGAAAGTA-----TCG 927
QY 95 GlyIleTyrSerProHisThrAlaTyrAspAlaIleProGlnIlyVal-----110
Db 928 GGCCTCCGAGAGCAGATCCAGAGCAAAAGTCCGACCTGCTCTGTGTGGCG 987
QY 111 -----AsnAsnTrpLeuAlaIlysgIlyLeuGlyAlaCysThrSerArgProIleHis 127
Db 988 CTTCGAGAGAGCGGCTGGCTTTCAAC-----CTTCGA 1020
QY 128 ProSerIlyAspAlaProAsnTyrProThrGluGlyAsnHisArgValGluPheAsnValAsn 147
Db 1021 GCCAGTGCATCCCTCAATAACCC-----TTCTCTATATCC 1056
QY 148 TyrThrGlnAspLeuAspIlyValIleMetSerAlaValIlysgIlyLeuAspIlyValSerVal 167
Db 1057 TACACGCTGCTGCACAGAC-----TCTTCTATATAGGTTG 1089
QY 168 ThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIleAsnLeuAsnCysThr 187
Db 1090 TTTCGAAACAGAGAGTGGCTTTAGCTCCGAAACCTTGAGCTATGAACTTCAGTTGCACA 1149
QY 188 GlnIlyAspAlaLeuMetGlnValValAspPhe-----197
Db 1150 GGGCCCATGTGTGCAAAATCGAGATTACAGCCAAATTGCTGCACAGCATCCAGGCTAC 1209
QY 198 -----LeuSerArgAsnIlysgIleuTyrGlnIlyThrGlu 209
Db 1210 TCATTGGAGATGTGAGAGATCTGGATTGGACACCATATACCATGTATGCGATCTATGAA 1269
QY 210 IleLeuSerLeuGluIlyProLeuLeuHisThrGlyMetGlyArgLeuCysThrIleu 229
Db 1270 ATGATACCAAGGAGAGAA-----CTCGTG 1293
QY 230 AspGluSerValSerLeuAlaThrMetIleAspArgIleAspArgHis-----245
Db 1294 ACAGACACCTACTCCCGAGATGATGACCAAGCAAGCAAGCAAGCAAGCC 1353
QY 246 ---LeuIlyLeuSerHisIleArgIleAlaLeuGlyValGlyArg-----ThrLeu 261
Db 1531 ---GGTTTGAATCTGCTCCCGCCCACTACAGCCCGCAGAGAGTGAAGCCGCAAG 1584

Db 1354 CTCCTCAAGGCCACGACGTCGGGAGCGTGGCTGTGATCCGCTACTGCTGGCTG 1413
QY GluSerGlnValValValAlaLeuCysAlaGlySerGlySerSerValLeuGlnGly 281
Db 1414 GAGAGAACGTCGCCCAAGGACGATGATGTTTGGGGGCGAGAGATGCGACAG 1473
QY 282 ValGlnAlaAspLeuThrGlyGlyMetSerHisAspThrLeuAspAlaAla 301
Db 1474 TTCGAGAGAGAAACAGTCTCTCCGCGACCGAGT---TTGAACCATCTGCTAGT 1530
QY 302 SerGlnGlyLeuAsnValIleLeuCysGlnHisSerAsnThrGlu-----ArgGly 318
Db 1531 -----GGTTGAATGCTGCCCTGGCCGACCTACAGCCGACCAAGAGCTGAACCGCAAG 1584
QY 319 PheLeuSerAspLeuArgAspMetLeuAspSer 329
Db 1585 CTGTCCTCAGATGAGATGTACTGCTGACTCT 1617
RESULT 13
US-09-328-352-3868
; Sequence 3868, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3868
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3868
Alignment Scores:
Pred. No.: 0.0433 Length: 1767
Score: 100.00 Matches: 80
Percent Similarity: 40.48% Conservative: 73
Best Local Similarity: 21.16% Mismatches: 119
Query Match: 5.56% Indels: 107
DB: 4 Gaps: 16
US-09-745-506-37 (1-350) x US-09-328-352-3868 (1-1767)
QY 24 AsnValGlyLeuLeuValGluProSerProHisThrValAsnThrLeuPheLeuThr 43
Db 424 AATAGTAATTCGTGCTGAGCT-----GTATTTGGAG 459
QY 44 AsnAspLeuThrGluGluValMetGluGlu-ValLeuGlnLysLysAlaAspLeu----- 61
Db 460 CACCATTAACTCGAAAAAGTTTACGACATTTTGCAGAGAAAGAGCGTTGACTTC 519
QY 62 -----IleLeuSerTyrHisProProIlePheArgProMetLysArgIleThr 77
Db 520 AATGATGAAGAGTTGATCTCGATGTTAATCTTGATGGCTCAACCGCTCAAGAGATG-- 577
QY 77 TrpAsnThrTrpLysGluArgLeuValIleArgAlaLeuGlnAsnArgValGlyIleTyr 97
Db 578 -----AAGAGAGCTCTCTCAAGCGATGAAGCCCGCCGATTTT-AAATA 620
QY 97 rSerProHisThrAlaTyrAspAlaAlaProGlnGlyValAsn----- 111
Db 621 TATTAATAGTATTATTAATGATGCATTCGATGGTCTTCAGACTTACATTTTGAAC 680
QY 111 ----- 111
Db 681 GTACAAAAATCCATTCGGGTCGCTATCGTGTGATGCTGTACGTAATTCGCA 740
QY 112 -----AsnTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgPr 125
Db 741 TCCCCCTCTACAGCTTGCAAAACGCTTGACATCAGCTTAAGTAATGTCTCAATGCA 800

QY 125 oIleHisProSerLysAlaPro-----AsnTrpProThrGlnGlyAsnH 140
Db 801 CATTTGCAAAAGCGCGCCCAAGATGTCGATACAGTCAAGCTCAAGCTCAAAAGCA 860
QY 140 sArgValGlnPheAsnValAsnTyrThrGlnAspLeu-----AspLysValMet----- 156
Db 861 AGCATGATGATTTGCTGAGACTCCCTCCGACTTGTGGTGAAGAAAGTATGTTACAG 920
QY 157 -----SerAlaValLysGlyIleAspGlyValSerValThrSerPhe 171
Db 921 TATTCCTGACCATCAAGCGCAATGCTAGAGATGATGACATA----- 963
QY 171 rAlaArgThrGlyAsnGlnGluGlnThrArgIleAsnLeuAsnGlyThrGlnLysAlaLe 191
Db 964 -----GGAATATGAAGAAGT-----CAAAAGCTTT 989
QY 191 uMetGlnValAlaAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGluIleLe 211
Db 990 GTTT-----ATGGAGCATATGATTAACCTCAAGCGCATGCTTTAATTAACCGACCAAC 1043
QY 211 uSerLeuGlnLysProLeuLeuLeuHisThrGlyMetGlyArgLeuCysThrLeuAspG 231
Db 1044 AGGTTCTGGTAACCCGATGCTATATACAGGTTTAATATTTTAATACT-----GA 1097
QY 231 uSerValSerLeuAlaThrMetIleAspArgIleLysArgHisLeuLys---LeuSerH 250
Db 1098 AAGTCGCAATATTTCTACTGCGGAAGACCGGTGAATTAACCTGAAGGATTAATCA 1157
QY 250 sIleArgLeuAlaLeuGlyValGlyArgThrLeuGlnSerGlnValValAlaLe 270
Db 1158 AGTTAACGTAACCCCAAGAGGCTTACTTTGCCGCCCACTTAA----- 1206
QY 270 uCysAlaGlySerGlySerSerValLeuGlnGlyValGluAlaAspLeuTyrLeuThrG 290
Db 1207 -----TCATTTTACG-----CAAGCCCTGACATTAATTAATGCTGG 1244
QY 290 yGluMetSerHisAspThr-----LeuAspAlaAlaSerGlnGlyLeas 306
Db 1245 TGAGATTCGTGACTTGGAAACAGCAGAAATTCGATTAAGCGCGCTCAAAACCGGCACAT 1304
QY 306 nValIleLeuCysGlnHisSerAsnThrGluArgGlyPheLeuSerAspLeuArgAspMe 326
Db 1305 GGTGATGCAACACTACTACTAATATGCTCCGGAACATTAAGACCGCTTACGTAATAT 1364
QY 326 t-----LeuAspSerHisLeuGlnAsnLysIleAsnIleLeuSerGlu 341
Db 1365 GGGGCTCTCTCTTTAATATTGCAACATCACTAAGTATTTGACAG 1416
RESULT 14
US-09-252-991A-12362/C
; Sequence 12362, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12362
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12362
Alignment Scores:
Pred. No.: 0.0318 Length: 969

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